```
cccccgccgtg agtgagctct caccccagtc agccaaatga gcctcttcgg gcttctcctg 60

gtgacatctg ccctggccgg ccagagacga gggactcagg cggaatccaa cctgagtagt 120

aaattccagt tttccagcaa caaggaacag aacggagtac aagatcctca gcatgagaga 180

attattactg tgtctactaa tggaagtatt cacagcccaa ggtttcctca tacttatcca 240

agaaatacgg tcttggtatg gagattagta gcagtagagg aaaatgtatg gatacaactt 300

acgtttgatg aaagatttgg gcttgaagac ccagaagatg acatatgcaa gtatgatttt 360

gtagaagttg aggaacccag tgatggaact atattagggc gctggtgtgg ttctggtact 420

gtaccaggaa aacagatttc taaaggaaat caaattagga taagatttgt atctgatgaa 480

tattttcctt ctgaaccagg gttctgcatc cactacaaca ttgtcatgcc acaattcaca 540

gaagctgtga gtccttcagt gctaccccct tcagctttgc cactggacct gcttaataat 600

gctataactg cctttagtac cttggaagac cttattcgat atcttgaacc agagagatgg 660

cagttggact tagaagatct atataggcca acttggcaac ttcttggcaa ggcttttgtt 720

tttggaagaa aatccagagt ggtggatctg aaccttctaa cagaggaggt aagattatac 780

agctgcacac ctcgtaactt ctcagtgtcc ataagggaag aactaaagag aaccgatacc 840

atttttctggc caggttgtct cctggttaaa cgctgtggtg ggaactgtgc ctgttgtctc 900

cacaattgca atgaatgtca atgtgtccca agcaaagtta ctaaaaaata ccacgaggtc 960

cttcagttga gaccaaagac cggtgtcagg ggattgcaca aatcactcac cgacgtggcc 1020

ctggagcacc atgaggagtg tgactgtgtg tgcagaggga gcacaggagg atagccgcat 1080

caccaccagc agctcttgcc catatctgtg cagtgcagtg gctgattcta ttagagaacg 1140

tatgcgttat ctccatcctt aatctcagtt gtttgcttca aggacctttc atcttcagga 1200
```

FIG. 1A

```
tttacagtgt attctgaaag aggagacatc aaacagaatt aggacttgtg caacagctct 1260

tttgagagga ggcctaaagg acaggagaaa aggtcttcaa tcgtggaaag aaaattaaat 1320

gttgtattaa atagatcacc agctagtttc agagtcacca tgtacgtatt ccactagctg 1380

ggttctgtat ttcagttctt tcgatacggc ttagggtaat gtcagtacag gaaaaaaact 1440

gtgcaagtga gcacctgatt ccgttgcctt gcttaactct aaagctccat gtcctgggcc 1500

taaaatcgta taaaatctgg atttttttt ttttttttgc tcatattcac atatgtaaac 1560

cagaacattc tatgtactac aaacctggtt tttaaaaagg aactatgttg ctatgaatta 1620

aacttgtgtc rtgctgatag gacagactgg attttcata tttcttatta aaatttctgc 1680

catttagaag aagagaacta cattcatggt ttggaagaga taaacctgaa aagaagagtg 1740

gccttatcct cactttatcg ataagtgact ttatttgttt cattgtgtac attttatat 1800

tctccttttg acattataac tgttggcttt tctaatcttg ttaaatatat ctatttttac 1860

caaaggtatt taatattctt ttttatgaca acttagatca actattttta gcttggtaaa 1920

tttttctaaa cacaattgtt atagccagag gaacaaagat ggatataaaa atattgttgc 1980

cctggacaaa aatacatgta tntccatccc ggaatggtgc tagagttgga ttaaacctgc 2040

attttaaaaa acctgaattg ggaanggaan ttggtaaggt tggccaaanc tttttgaaa 2100

ataattaa                                                      2108
```

FIG. 1B

```
Met Ser Keu Phe Gly Leu Leu Leu Cal Thr Ser Ala Leu Ala Gly Gln
  1               5                    10                   15
Arg Arg Gly Thr Gln Ala Glu Ser Asn Leu Ser Ser Lys Phe Gln Phe
            20                   25                   30
Ser Ser Asn Lys Glu Gln Asn Gly Val Gln Asp Pro Gln His Glu Arg
        35                   40                   45
Ile Ile Thr Val Ser Thr Asn Gly Ser Ile His Ser Pro Arg Phe Pro
     50                   55                   60
His Thr Tyr Pro Arg Asn Thr Val Leu Val Trp Arg Leu Val Ala Val
 65                   70                   75                   80
Glu Glu Asn Val Trp Ile Gln Leu Thr Phe Asp Glu Arg Phe Gly Leu
               85                   90                   95
Glu Asp Pro Glu Asp Asp Ile Cys Lys Gly Asp Phe Val Glu Val Glu
            100                  105                  110
Glu Pro Ser Asp Gly Thr Ile Leu Gly Arg Trp Cys Gly Ser Gly Thr
        115                  120                  125
Val Pro Gly Lys Gln Ile Ser Lys Gly Asn Gln Ile Arg Ile Arg Phe
    130                  135                  140
Val Ser Asp Glu Tyr Phe Pro Ser Glu Pro Gly Phe Cys Ile His Tyr
145                  150                  155                  160
Asn Ile Val Met Pro Gln Phe Thr Glu Ala Val Ser Pro Ser Val Leu
            165                  170                  175
Pro Pro Ser Ala Leu Pro Leu Asp Leu Leu Asn Asn Ala Ile Thr Ala
        180                  185                  190
Phe Ser Thr Leu Glu Asp Leu Ile Arg Tyr Leu Glu Pro Glu Arg Trp
        195                  200                  205
Gln Leu Asp Leu Glu Asp Leu Tyr Arg Pro Thr Trp Gln Leu Leu Gly
    210                  215                  220
Lys Ala Phe Val Phe Gly Arg Lys Ser Arg Val Val Asp Leu Asn Leu
225                  230                  235                  240
Leu thr Glu Glu Val Arg Leu Tyr Ser Cys Thr Pro Arg Asn Phe Ser
            245                  250                  255
Val Ser Ile Arg Glu Glu Leu Lye Arg Thr Asp Thr Ile Phe Trp Pro
            260                  265                  270
Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala Cys Cys Leu
        275                  280                  285
```

FIG. 2A

His Asn Cys Asn Glu Cys Gln Cys Val Pro Ser Lys Val Thr Lsy Lys
    290   295   300

Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr Gly Cal Arg Gly Leu
305   310   315   320

His Lys Ser Leu Thr Asp Val Ala Leu Glu His His Glu Glu Cys Asp
          325   330   335

Cys Val Cys Arg Gly Ser Thr Gly Gly
        340   345

FIG. 2B

```
cgggtaaatt ccagttttcc agcaacaagg aacagaacgg agtacaagat cctcagcatg 60
agagaattat tactgtgtct actaatggaa gtattcacag cccaaggttt cctcatactt 120
atccaagaaa tacggtcttg gtatggagat tagtagcagt agaggaaaat gtatggatac 180
aacttacgtt tgatgaaaga tttgggcttg aagacccaga agatgacata tgcaagtatg 240
attttgtaga agttgaggaa cccagtgatg gaactatatt agggcgctgg tgtggttctg 300
gtactgtacc aggaaaacag atttctaaag gaaatcaaat taggataaga tttgtatctg 360
atgaatattt tccttctgaa ccaggggttct gcatccacta caacattgtc atgccacaat 420
tcacagaagc tgtgagtcct tcagtgctac cccttcagc tttgccactg gacctgctta 480
ataatgctat aactgccttt agtaccttgg aagaccttat tcgatatctt gaaccagaga 540
gatggcagtt ggacttagaa gatctatata ggccaacttg gcaacttctt ggcaaggctt 600
ttgttttttgg aagaaaatcc agagtggtgg atctgaacct tctaacagag gaggtaagat 660
tatacagctg cacacctcgt aacttctcag tgtccataag ggaagaacta aagagaaccg 720
ataccatttt ctggccaggt tgtctcctgg ttaaacgctg tggtgggaac tgtgcctgtt 780
gtctccacaa ttgcaatgaa tgtcaatgtg tcccaagcaa agttactaaa aaataccacg 840
aggtccttca gttgagacca aasaccggtg tcagggggatt gcacaaatca ctcaccgacg 900
tggccctgga gcaccatgag gagtgtgact gtgtgtgtag agggagcaca ggaggatagc 960
cgcatcacca ccagcagctc ttgcccagag ctgtgcagtg cagtggctga ttctattaga 1020
gaacgtatgc gttatctcca tccttaatct cagttgtttg cttcaaggac ctttcatctt 1080
caggatttac agtgcattct gaaagaggag acatcaaaca gaattaggag ttgtgcaaca 1140
gctcttttga gaggaggcct aaaggacagg agaaaaggtc ttcaatcgtg gaaagaaaat 1200
taaatgttgt attaaataga tcaccagcta gtttcagagt taccatgtat gtattccact 1260
agctgggttc tgtatttcag ttctttcgat acggcttagg gtaatgtcag tacaggaaaa 1320
aaactgtgca agtgagcacc tgattccgtt gccttgctta actctaaagc tccatgtcct 1380
gggcctaaaa tcgtataaaa tctggatttt tttttttttt tttgctcata ttcacatatg 1440
taaaccagaa cattctatgt actacaaacc tggtttttaa aaaggaacta tgttgctatg 1500
aattaaactt gtgtcatgct gataggacag actgga                            1536
```

FIG.3

```
Gly Lys Phe Gln Phe Ser Ser Asn Lys Glu Gln Asn Gly Val Gln Asp
 1               5                  10                      15
Pro Gln His Glu Arg Ile Ile Thr Val Ser Thr Asn Gly Ser Ile His
               20                  25                      30
Ser Pro Arg Phe Pro His Thr Tyr Pro Arg Asn The Val Leu Val Trp
         35                  40                  45
Arg Leu Val Ala Val Glu Glu Asn Val Trp Ile Gln Leu Thr Phe Asp
     50                  55                  60
Glu Arg Phe Gly Leu Glu Asp Pro Glu Asp Asp Ile Cys Lys Tyr Asp
 65                  70                  75                      80
Phe Val Glu Val Glu Glu Pro Ser Asp Gly The Ile Leu Gly Arg Trp
                 85                  90                  95
Cys Gly Ser Gly Thr Val Pro Gly Lys Gln Ile Ser Lys Gly Asn Gln
             100                 105                 110
Ile Arg Ile Arg Phe Val Ser Asp Glu Tyr Phe Pro Ser Glu Pro Gly
         115                 120                 125
Phe Cys Ile His Tyr Asn Ile Val Met Pro Gln Phe Thr Glu Ala Val
     130                 135                 140
Ser Pro Ser Val Leu Pro Pro Ser Ala Leu Pro Leu Asp Leu Leu Asn
145                 150                 155                 160
Asn Ale Ile Thr Ala Phe Ser Thr Leu Glu Asp Leu Ile Arg Tyr Leu
             165                 170                 175
Glu Pro Glu Arg Trp Gln Leu Asp Leu Glu Asp Leu Tyr Arg Pro Thr
             180                 185                 190
Trp Gln Leu Leu Glu Lys Ala Phe Val Phe Gly Arg Lys Ser Arg Val
         195                 200                 205
Val Asp Leu Asn Leu Leu Thr Glu Glu Val Arg Leu Tyr Ser Cys Thr
     210                 215                 220
Pro Arg Asn Phe Ser Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp
225                 230                 235                 240
the Ile Phe Trp Pro Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn
             245                 250                 255
Cys Ala Cys Cys Leu His Asn Cys Asn Glu Cys Gln Cys Val Pro Ser
             260                 265                 270
Lys Val Thr Lys Lys Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr
     275                 280                 285
Gly Val Arg Gly Leu His Lys Ser Leu Thr Asp Val Ala Leu Glu His
     290                 295                 300
His Glu Glu Cys Asp Cys Val Cys Arg Gly Ser Thr Gly Gly
305                 310                 315
```

FIG.4

```
cacctggaga cacagaagag ggctctagga aaaatttttgg atgggggatta tgtggaaact 60
accctgcgat tctctgctgc cagagccggc caggcgcttc caccgcagcg cagcctttcc 120
ccgggctggg ctgagccttg gagtcgtcgc ttccccagtg cccgccgcga gtgagccctc 180
gccccagtca gccaaatgct cctcctcggc cctcctcggc ctcctcctgc gctggccggc 240
caaagaacgg ggactcgggc tgagtccaac ctgagcagca agttgcagct ctccagcgac 300
aaggaacaga acggagtgca agatccccgg catgagagag ttgtcactat atctggtaat 360
gggagcatcc acagcccgaa gtttcctcat acgtacccaa gaaatatggt gctggtgtgg 420
agattagttg cagtagatga tatagtgcgg atccagctga catttgatga gagatttggg 480
ctggaagatc cagaagacga tatatgcaag tatgattttg tagaagttga ggagcccagt 540
gatggaagtg ttttaggacg ctggtgtggt tctgggactg tgccaggaaa gcagacttct 600
aaaggaaatc atatcaggat aagatttgta tctgatgagt attttccatc tgaacccgga 660
ttctgcatcc actacagtat tatcatgcca caagtcacag aaaccacgag tccttcggtg 720
ttgccccctt catctttgtc attggacctg ctcaacaatg ctgtgactgc cttcagtacc 780
ttggaagagc tgattcggta cctagagcca gatcgatggc aggtggactt ggacagcctc 840
tacaagccaa catggcagct tttgggcaag gctttcctgt atgggaaaaa aagcaaagtg 900
gtgaatctga atctcctcaa ggaagaggta aaactctaca gctgcacacc ccggaacttc 960
tcagtgtcca tacgggaaga gctaaagagg acagatacca tattctggcc aggttgtttt 1020
ctggtcaagt gctgtggagg aaattgtgcc tgttgtctcc ataattgcaa tgaatgtcag 1080
tgtgtcccac gtaaagttac aaaaaagtac catgaggtcc ttcagttgag accaaaaact 1140
ggagtcaagg gattgcataa gtcactcact gatgtggctc tggaacacca cgaggaatgt 1200
gactgtgtgt gtagaggaaa cgcaggaggg taactgcagc cttcgtagca gcacacgtga 1260
gcactggcat tctgtgtacc cccacaagca accttcatcc ccaccagcgt tggccgcagg 1320
gctctcagct gctgatgctg gctatggtaa agatcttact cgtctccaac caaattctca 1380
gttgtttgct tcaatagcct tcccctgcag gacttcaagt gtcttctaaa agaccagagg 1440
caccaanagg agtcaatcac aaagcactgc accg                               1474
```

FIG.5

```
Met Leu Leu Leu Gly Leu Leu Leu Leu Thr Ser Ala Leu Ala Gly Gln
 1               5                      10                      15

Arg Thr Gly Thr Arg Ala Glu Ser Asn Leu Ser Ser Lys Leu Gln Leu
            20                      25                      30

Ser Ser Asp Lys Glu Gln Asn Gly Val Gln Asp Pro Arg His Glu Arg
        35                      40                      45

Val Val Thr Ile Ser Gly Asn Gly Ser Ile His Ser Pro Lys Phe Pro
    50                      55                      60

His Thr Tyr Pro Arg Asn Met Val Leu Val Trp Arg Leu Val Ala Val
65                      70                      75                  80

Asp Glu Asn Val Arg Ile Gln Leu Thr Phe Asp Glu Arg Phe Gly Leu
                85                      90                      95

Glu Asp Pro Glu Asp Asp Ile Cys Lys Tyr Asp Phe Val Glu Val Glu
            100                     105                     110

Glu Pro Ser Asp Gly Ser Val Leu Gly Arg Trp Cys Gly Ser Gly Thr
        115                     120                     125

Val Pro Gly Lys Gln Thr Ser Lys Gly Asn His Ile Arg Ile Arg Phe
    130                     135                     140

Val Ser Asp Glu Tyr Phe Pro Ser Glu Pro Gly Phe Cys Ile His Tyr
145                     150                     155                 160

Ser Ile Ile Met Pro Gln ValThr Glu Thr Thr Ser Pro Ser Val Leu
                165                     170                     175

Pro Pro Ser Ser Leu Ser Lei Asp Leu Leu Asn Asn Ala Val Thr Ala
            180                     185                     190

Phe Ser Thr Leu Glu Glu Leu Ile Arg Tyr Leu Glu Pro Asp Arg Trp
        195                     200                     205

Gln Val Asp Leu Asp Ser Leu Tyr Lys Pro Thr Trp Gln Leu Leu Gly
    210                     215                     220

Lys Ala Phe Leu Tyr Gly Lys Lys Ser Lys Val Val Asn Leu Asn Leu
225                     230                     235                 240

Leu Lys Glu Glu Val Lys Leu Tyr Ser Cys Thr Pro Arg Asn Phe Ser
            245                     250                     255

Val Ser Ile Arg Glu Glu Leu Lys Arg Thr Asp Thr Ile Phe Trp Pro
        260                     265                     270

Gly Cys Leu Leu Val Lys Arg Cys Gly Gly Asn Cys Ala Cys Cys Leu
    275                     280                     285
```

FIG. 6A

```
His Asn Cus Asn Glu Cys Gln Cys Val Pro Arg Lys Val Thr Lys Lys
    290                 295                 300
Tyr His Glu Val Leu Gln Leu Arg Pro Lys Thr Gly Val Lys Gly Leu
305                 310                 315                 320
His Lys Ser Leu Thr Asp Val Ala Leu Glu His His Glu Glu Cys Asp
            325                 330                 335
Cys Val Cys Arg Gly Asn Ala Gly Gly
            340                 345
```

FIG. 6B

```
hPDGF-C  MSLFGLLLVTSALAGQRRGTQAESNLSSKFQFSSNKEQNG  40
mPDGF-C  MLLLGLLLITSALAGQRTGTRRESNLSSKLQLSSQKEQNG  40

hPDGF-C  VQQPQHERLLTVSTNGSIHSPPFPHTYFRNTVLVNRLVAV  80
mPDGF-C  VQDPRMERVVTISGNGSTHSRKFPHTYFRNMVLVNRLVAV  80

hPDGF-C  FENVNIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTTS  120
mPDGF-C  GENVRTQLTFDERFGLEDPEDDICEYDFVEVEEPSDGSVS  120

hPDGF-C  GRWCGSGTVFGKQISKGNQIRIRFVSDEYFPSEPGFCIHY  160
mPDGF-C  GRWCGSGTVFGKQTSKGNHIRIRFVSDEYEPSEPGFCIHY  160

hPDGF-C  NIVMPQFTEAVSPSVLPPSSLPLDLLNNAITAFSTLFDLI  200
mPDGF-C  SITMPQVTETTSPSVLPPSSLSLDLLNNAVTAFSTLFDLI  200

hPDGF-C  RYLEPFRWQLPLEQLYEFTWQLLCKAFVFGRKSRVVDLNL  240
mPDGF-C  RYLEPDPWQVPLPSLYKPTWQLLGFAFLYGKKSNVVNLNL  240

hPDGF-C  LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGGLLVKRC  280
mPDGF-C  LKFFVKLYSCTPRNFSVSIREELKRTDTIFWPGGLLVKRC  280

hPDGF-C  GGNCACCLRNCNECQCVPSKVTKKYHEVLQLRPKTGVRGY  320
mPDGF-C  GGNCACCLRVCNECQCVPRKVTKKYHEVLQLRPKTGVRGY  320

hPDGF-C  HESLTDVALEHHEECDCVCRGSTGG  345
mPDGH-C  HESLTDVALEHHEECDCVCRGNAGG  345
```

FIG.7
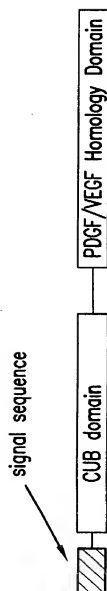
FIG.8
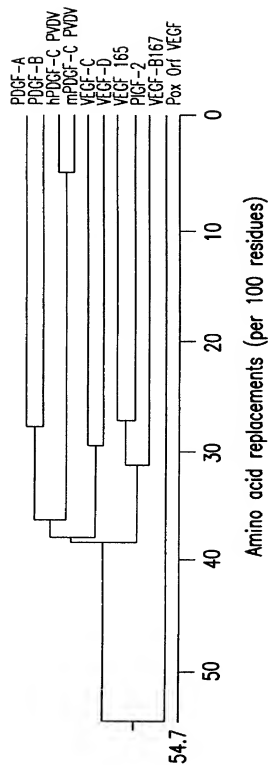
FIG.10

```
VEGF 165      - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   1
PlGF-2        - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   1
VEGF-B167     - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   1
Pgx Crf VEGF  - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   1
VEGF-C        M H L L G F F S V A C S L L A A A L L P G P R E A P A A A A  30
VEGF-D        - - - - - - - - - - - - - - - M Y G E W G M G N I L M M F H  15
PDGF-A        - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   1
PDGF-B        - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   1
hPDGF-C PVDV  - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   1
mPDGF-C PVDV  - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   1


VEGF 165      - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   1
PlGF-2        - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   1
VEGF-B167     - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   1
Pox Orf VEGF  - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   1
VEGF-C        A F E S G L D L S D A E P D A G E A T A Y A S K D L E E Q L  60
VEGF-D        V Y L V O G F R S E H G P Y K D F S F E R S S R S M L E R S  45
PDGF-A        - - - - M R T L A C L L L L G C G Y L A N V L A E E A E I P  26
PDGF-B        M N R C W A L F L S L C C Y L R L V S A E G D P I P E E L Y  30
hPDGF-C PVDV  - - - - - - M P Q F T E A V S P S V L P P S A L P L D L L  23
mPDGF-C PVDV  - - - - - - M P Q V T E T T S P S V L P P S A L S L D L L  23


VEGF 165      - - - - - - - - - - - - - - - - - - M N F L L S W V E W  10
PlGF-2        - - - - - - - - - - - - - - - - - - M P V M R L F P C F  10
VEGF-B167     - - - - - - - - - - - - - - - - - - - - - M S P L L   5
Pox Orf VEGF  - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -   1
VEGF-C        R S V S S V D E L M T V L Y P E Y W K M Y K C Q L R K G G W  90
VEGF-D        E O O I R A A S S L E E L L O I A H S E D W K L W R C R L K  75
PDGF-A        R E V I E R L A R S Q I H S I R D L Q R L L E I D S V G S E  56
PDGF-B        E M L S D H S I R S F D D L O R L L H G D P - - - - - G E E  55
hPDGF-C PVDV  N N A I T A F S T L E D L I R Y L E P E R W Q L D L E D L Y  53
mPDGF-C PVDV  N N A V T A F S T L E E L I R Y L E P D R W Q V D L D S L Y  53


VEGF 165      S L A L L L Y L H H A K W S Q A A P M A E G G G Q N H H E V  40
PlGF-2        L Q L L A G L A L P A V P P Q Q W A L S A G N G S S E V E V  40
VEGF-B167     R R L L L A A L L Q L A P A Q A P V S Q P D A P G H Q R K V  35
Pox Orf VEGF  - - - - - M K L L V G I L V A V C L H Q Y L L N A D S N T  24
VEGF-C        Q H N R E Q A N L N S R T E E T I K F A A A H Y N T E I - L 119
VEGF-D        L K S L A S M D S R S A S H R S T R F A A T F Y D T E T - L 104
PDGF-A        D S L D T S L R A H G V H - - A T K H V P E K R P L R I R R  84
PDGF-B        D G A E L D L N M T R S H S G G E L E S L A R G R R S L G S  85
hPDGF-C PVDV  R P T W Q L L G K A F V F G R K S R - - - - - - - - V V D L  75
mPDGF-C PVDV  K P T W Q L L G K A F L Y G K K S K - - - - - - - - V V N L  75
```

FIG. 9A

```
VEGF 165     V K F M D V Y O R S Y C H P I E T L V D I F Q E Y P D E I E   70
PlGF-2       V P F Q E V W G R S Y C R A L E R L V D V V S E Y P S E V E   70
VEGF-B167    V S W I D V Y T R A T C Q P R E V V V P L T V E L M G T V A   65
Pox Orf VEGF K G W S E V L K G S E C K P R P I V V P V S E T H P E L T S  54
VEGF-C       K S I D N E W R K T Q C M P R E V C I D V G K E F G V A T N  149
VEGF-D       K V I D E E W D R T Q C S P R E T C V E V A S E L G K T T N  134
PDGF-A       K R S I E E A V P A V C K T R T V I Y E I P R S Q V D P T S  114
PDGF-B       L T I A E P A M I A E C K T R T E V F E I S R R L I D R T N  115
HPDGF-C PVDV N L L T E E V R L Y S C T P R N F S V S I - R E E L K R T D 104
mPDGF-C PVDV N L L K E E V K L Y S C T P R N F S V S I - R E E L K R T D 104

VEGF 165     Y I F K - - P S C V P L M R C G G - - - C C N D E G L E C V    95
PlGF-2       H M F S - - P S C V S L L R C T G - - - C C G D E D L H C V    95
VEGF-B167    K Q L V - - P S C V T V Q R C G G - - - C C P D D G L E C V    90
Pox Orf VEGF Q R F N - - P P C V T L M R C G G - - - C C N D E S L E C V  79
VEGF-C       T F F K - - P P C V S V Y R C G G - - - C C N S E G L Q C M   174
VEGF-D       T F F K - - P P C V N V F R C G G - - - C C N E E G V M C M   159
PDGF-A       A N F L I W P P C V E V K R C T G - - - C C N T S S V K C Q   141
PDGF-B       A N F L V W P P C V E V Q R C S G - - - C C N N R N V Q C R   142
hPDGF-C PVDV T I F - - W P G C L L V K R C G G N C A C C L H N C N E C Q 132
mPDGF-C PVDV T I F - - W P G C L L V K R C G G N C A C C L E N C N E C Q 132

VEGF 165     P T E E S N I T M Q I M R I K - - - P H Q G Q - - - - - H I  117
PlGF-2       P V E T A N V T M Q L L K I R - - - S G D R P - - - - - S Y  117
VEGF-B167    P T G Q H Q V R M Q I L M I R Y - - P S S Q L - - - - - - -  111
Pox Orf VEGF P T E E V N V S M E L L G A S G S G S N G M Q - - - - - R L 104
VEGF-C       N T S T S Y L S K T L F E I T V - - P L S Q G - - - - - P K  197
VEGF-D       N T S T S Y I S K O L F E I S V - - P L T S V - - - - - P E  182
PDGF-A       P S R V H H R S V K V A K V E Y V R K K P K L - - - - - K E  166
PDGF-B       P T Q V Q L R P V Q V R K L E I V R K K P I F - - - - - K K  167
hPDGF-C PVDV C V P - S K V T K K Y H E V L Q L R P K T G V R G L H K S L 161
mPDGF-C PVDV C V P - R K V T K K Y H E V L Q L R P K T G V K G L H K S L 161

VEGF 165     G E M S F L Q H N K - C E C R P K K - - - - - - - - - - D R  136
PlGF-2       V E L T F S Q H V R - C E C R P L R E - - - - K M K P E R R  142
VEGF-B167    G E M S L E E H S Q - C E C R P K K K - - - - - D S A V K P  135
Pox Orf VEGF S F V E H K K - - - - C D C R P R F T - - - - - - - T T P P 123
VEGF-C       P V T I S F A N H T S C R C M S K L D - - - V Y R Q V H S I  224
VEGF-D       L V P V K I A N H T G C K C L P T G P - - - - R H P Y S I   207
PDGF-A       V Q V R L E E H L E - C A C A T T S L N P D Y R E E D T G R  195
PDGF-B       A T V T L E D H L A - C K C E T V A A A R P V T R S P G G S  196
hPDGF-C PVDV T D V A L E H H E E - C D C V C R G S T G G                 182
mPDGF-C PVDV T D V A L E H H E E - C D C V C R G N A G G                 182
```

FIG. 9B

```
VEGF 165     A R Q E N P C G P C S S E R R K H L F V Q D P Q T C K C S C   166
PIGF-2       R P K G R G K R R R E N Q R P T D C H L C G D A V P R R         170
VEGF-B167    D S P R P L C P R C T Q H H Q R P D P R T - - - - C R C R C     161
Pox Orf VEGF T T T R P P R R R R                                           133
VEGF-C       I R R S L R A T - L P Q C Q A A N K T C P T N Y M W N N H I    253
VEGF-D       I R R S L O T P E E D E C P H S K K L C P I D M L W D N T K    236
PDGF-A       P R E S G K K R K R K R L K P T                                211
PDGF-B       Q E Q R A K T P Q T R V T I R T V R V R R P P K G K H R K F    225
hPDGF-C PVDV                                                               182
mPDGF-C PVDV                                                               182


VEGF 165     K N T D S - R C K A R Q L E L N E R T C R C D K P R R          192
PIGF-2                                                                     170
VEGF-B167    R R R S F L R C Q G R G L E L N P D T C R C R K L R R          188
Pox Orf VEGF                                                               133
VEGF-C       C R C L A Q E D F M F S S D A G D D S T D G F H D I C G P N    283
VEGF-D       C K C V L O D E - T P L P G T E D H S Y L O E P T L C G P H    266
PDGF-A                                                                     211
PDGF-B       K H T H D K T A L K E T L G A                                 241
hPDGF-C PVDV                                                               182
mPDGF-C PVDV                                                               182


VEGF 165                                                                   192
PIGf-2                                                                     170
VEGF-B167                                                                  188
Pox Orf VEGF                                                               133
VEGF-C       K E L D E E T C Q C V C R A G L R P A S C G P H K E L D R N    313
VAGF-D       M T F D E D R - - - - - - - - - - - - - - - - - - - - - - -   273
PDGF-A                                                                     211
PDGF-B                                                                     241
hPDGF-C PVDV                                                               182
mPDGF-C PVDV                                                               182


VEGF 165                                                                   192
PIGF-2                                                                     170
VEGF-B167                                                                  188
Pox Orf VEGF                                                               133
VEGF-C       S C Q C V C K N K L F P S Q C G A N R E F D E N T C Q C V C    343
VEGF-D       - C E C V C K A P C P G D L I O H P E N - - - - - C S C F E    297
PDGF-A                                                                     211
PDGF-B                                                                     241
hPDGF-C PVDV                                                               182
mPDGF-C PVDV                                                               182
```

FIG. 9C

VEGF 165		192
PIGF-2		170
VEGF-B167		188
Pox Orf VEGF		133
VEGF-C	K R T C P R N Q P L N P G K C A C E C T E S P Q K C L L K G	373
VEGF-D	C K E S L E S C C O K K K I - - - - - - - - - - - - - -	312
PDGF-A		211
PDGF-B		241
hPDGF-C PVDV		182
mPDGF-C PVDV		182

VEGF 165		192
PIGF-2		170
VEGF-B167		188
Pox Orf VEGF		133
VEGF-C	K K F H H Q T C S C Y R R P C T N R Q K A C E P G F S Y S E	403
VEGF-D	- - F H P D T C S C E D R - C P F H T R T C A S R K P A C G	338
PDGF-A		211
PDGF-B		241
hPDGF-C PVDV		182
mPDGF-C PVDV		182

VEGF 165		192
PIGF-2		170
VEGF-B167		188
Pox Orf VEGF		133
VEGF-C	E V C R C V P S Y W K R P Q M S	419
VEGF-D	K H W R F P K E T R A Q G L Y S O E N P	358
PDGF-A		211
PDGF-B		241
hPDGF-C PVDV		182
mPDGF-C PVDV		182

FIG. 9D

FIG. 11

Sequence alignment (CUB domains):

```
mPDGF-C CUB    ERVVTISGNGSIHSPKFPHTYPRNMVLVWRLVAVDENVRI  85
hPDGF-C CVB    ERITTIVSTNGSIHSPRFPHTYPRNTVLVWRLAVIENVWI  59
hBMP-1 CUB1    CGGDVKKDYGNTQSPNYPQDYRPSKVCIWRIOVSEGF-HV  360
hBMP-2 CUB3    CGGFLTKLNGSITTSPGCWPIXEYPNKNCIIWQLVAPTQY-RI  473
Neuropilin CUB1 CDTIKIIESPICYLTSPGYPMSIYHPSEKCEWLIQAPDPYQRI  629
Neuropilin CUB2 CSQNYTTPSGVIKSPGFPIEEYPNSLCCTYIVPAPXMSE-TI  67/195

mPDGF-c cub    QLTFDERDGLED----PEDDOCKYDPVEVEEI--PSDGSVLI  120
hPDGF-C CUB    QLTFDERFGLED----PEDDICKYDFVEVEEI--PSDGTILI  93
hBMP-1 CUB1    LNFTS-DLYRSA----LCWNDYDYIEVRDGHSGLLR  393
hBMP-1 CUB2    GLTFQS-FETERND--SCAYDDYLEVRDGENSSTL-H  506
hBMP-1 CUB3    SLQFDF-FETEGND--VCKYDFVEVRSGLTADSKLH  662
Neuropilin CUB1 MINFNPHFDLEDRD--CKYDFLHITWDGFPDVGPHI  100
Neuropilin CUB2 ILEEFES-FDLEPDSNPPCCWFCRYDRLHITWDGFPDVGPHI  224

mPDGF-C CUB    GRWCCSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCIHY  160
hPDGF-C CUB    GRWCCSGTVPGEOITSKCGNQIRIRFVSDEYFPSNWVGK-HI  133
hBMP-1 CUB1    CRFCCGSI-KLIPEPIVSITDSRLWVEFRSSSNWVGK-GFFAVNY  431
hBMP-1 CUB2    GRIYCCGSI-Y--EKPDDIKISTSSRLWLKFVSDGSINKK-GFAVNY  544
hBMP-1 CUB3    GKFCCGSI-EKPEVIITSQYNNMRVEFXSDNTVSKK-GFKAHF  700
Neuropilin CUB1 GKFCCGK--IAPPVVISGPFLFIKFVSDYETKGA-GFSIRY  138
Neuropilin CUB2 GKYCCGQ-KTPGRIRSSGILSMVFYTDSAIAKE-GFSANY  262

mPDGF-C CUM    STI                                      163
hPDGF-C CUB    MIV                                      136
hBMP-1 CUB1    EAII                                     434
hBMP-1 CUB2    FK                                       546
hBMP-1 CUB3    FSE                                      703
Neuropilin CUB1 -ETI                                    140
Neuropilin CUB2 SVL                                     265
```

FIG. 12
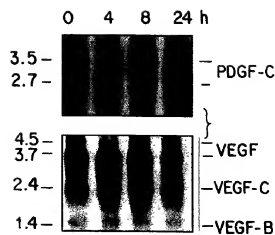
FIG. 13
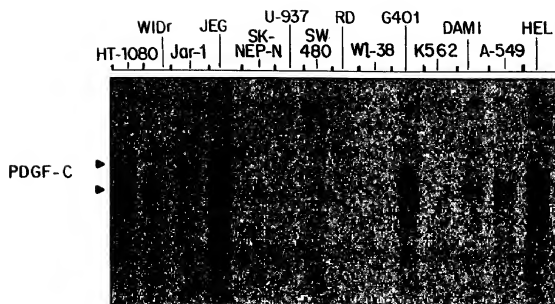
FIG.14
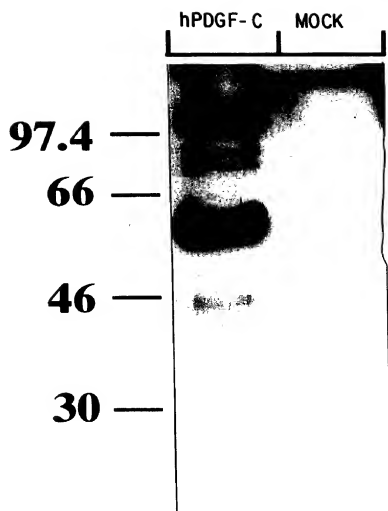
FIG. 15
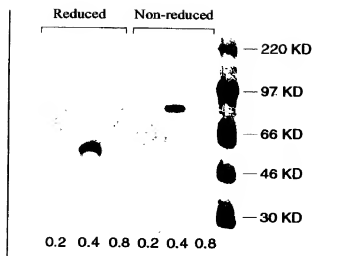
FIG. 16A
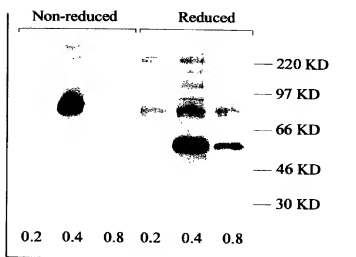
FIG. 16B
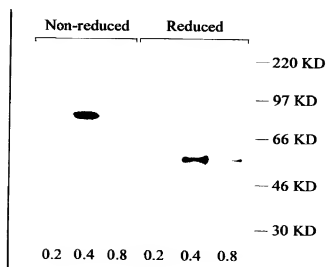
FIG. 16C
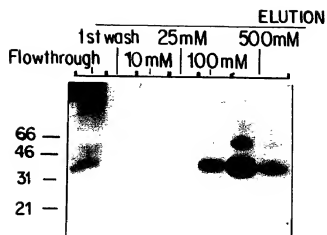
FIG. 17A
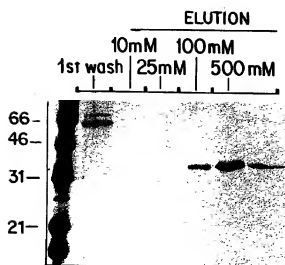
FIG. 17B
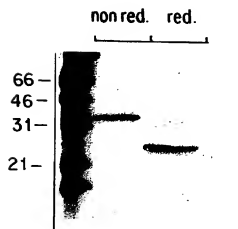
FIG. 17 C
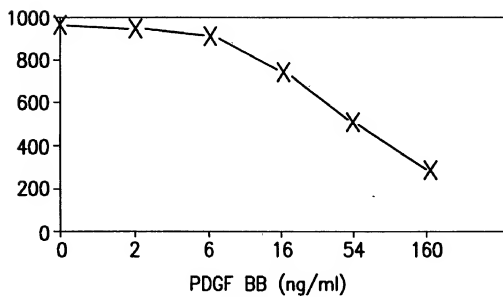
FIG. 18
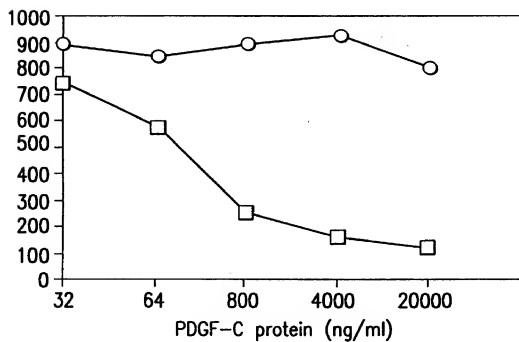
FIG. 19
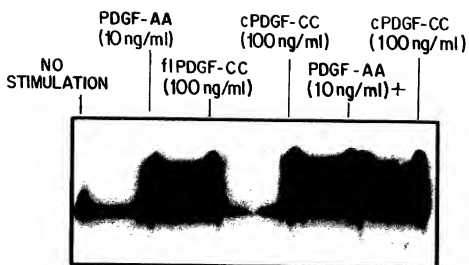
IP: PDGF alpha-rec.
IB: P-T yr

FIG. 20

FIG. 21

FIG. 22

INTACT
PDGF-C

PLASMIN-
DIGESTED PDGF-C

— 55

— 26 - 28
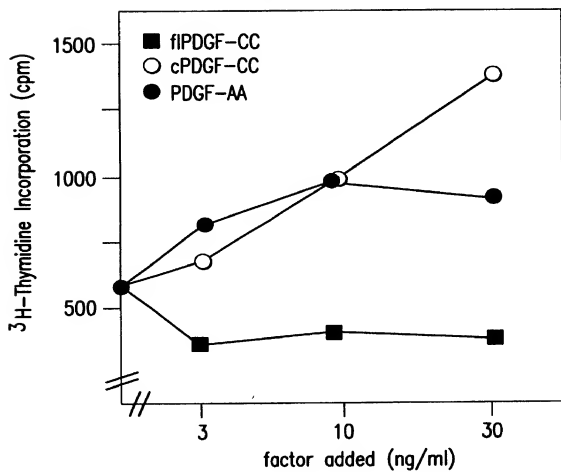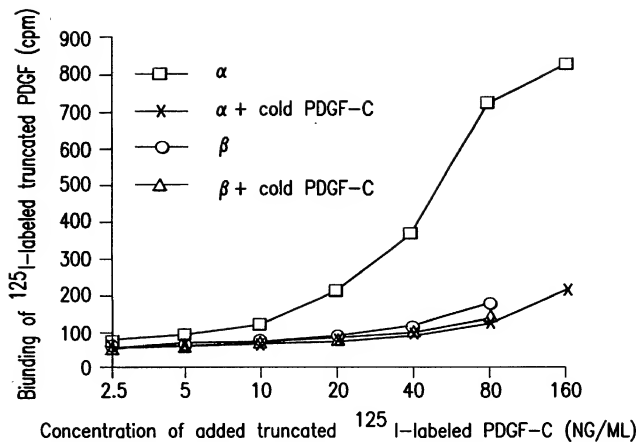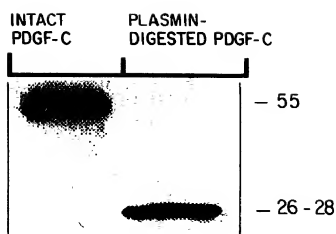
FIG. 23
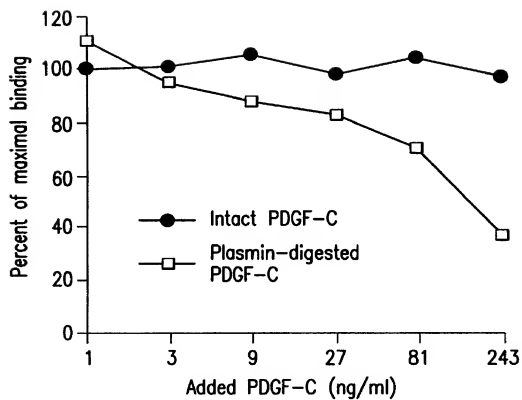
FIG. 24
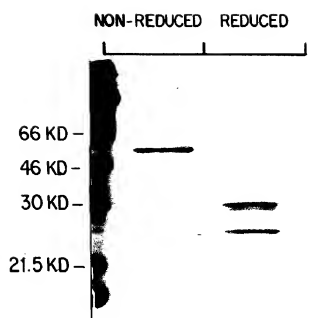
FIG. 25

FIG. 26A
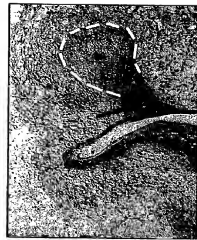
FIG. 26B

FIG. 26C
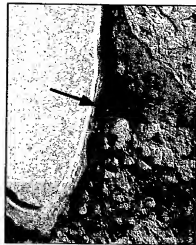
FIG. 26D

FIG. 26E
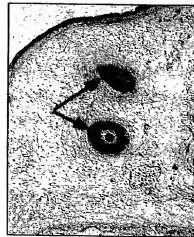
FIG. 26F
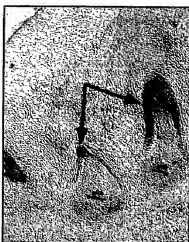
FIG.26 I
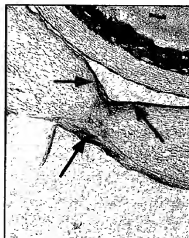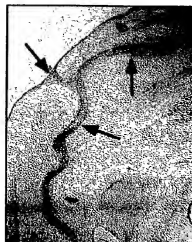
FIG.26H

FIG.26 G

FIG. 26L
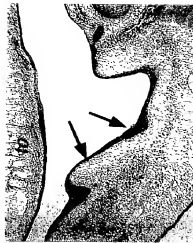
FIG. 26K

FIG. 26 J

FIG. 26 O

FIG. 26N
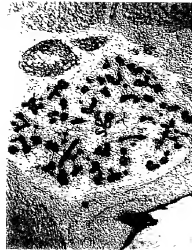
FIG. 26 M

FIG. 26 Q
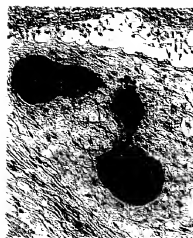
FIG. 26P

FIG. 26 R

FIG. 26S

FIG. 26T
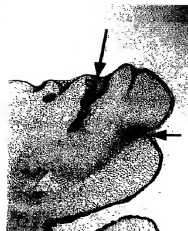
FIG. 26U

FIG. 26 V

FIG. 27B
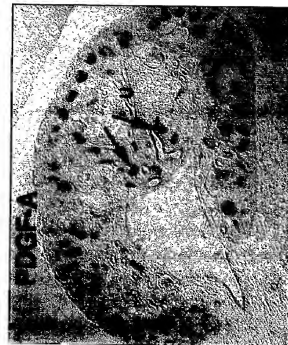
FIG. 27D
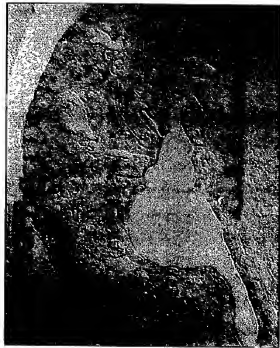
FIG. 27A

FIG. 27C

FIG.27E

FIG. 27F

FIG. 28A

PDGFR-α -/-
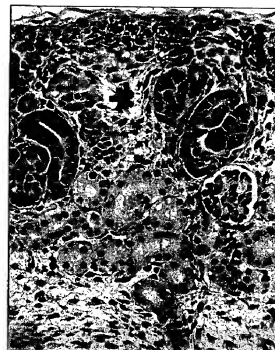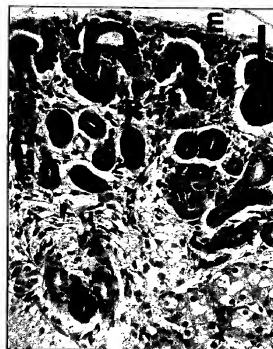
FIG. 28B

FIG. 28C

FIG. 28D
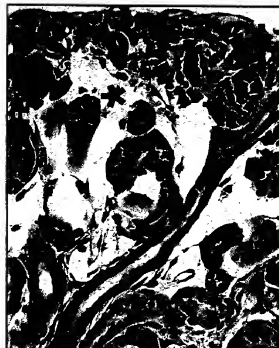
FIG. 28E
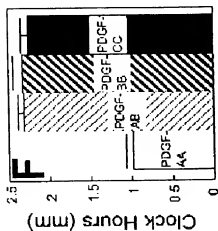

FIG. 28F
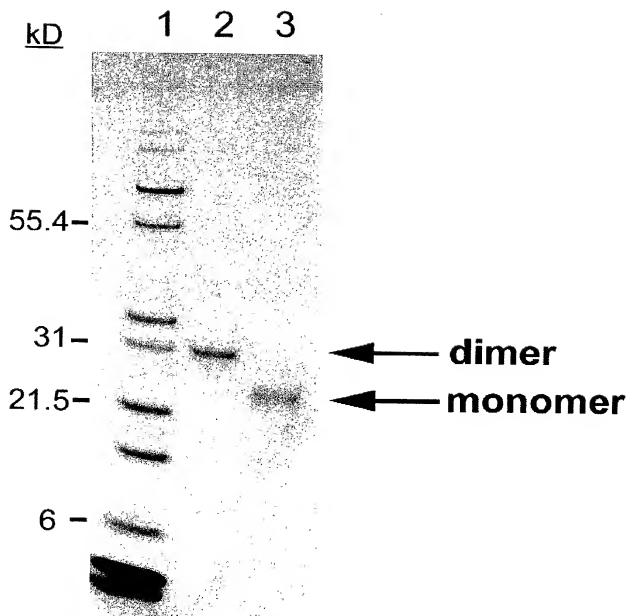
FIG. 29
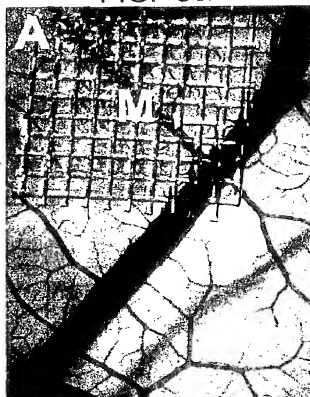
FIG. 30A

FIG. 30B

FIG. 30C
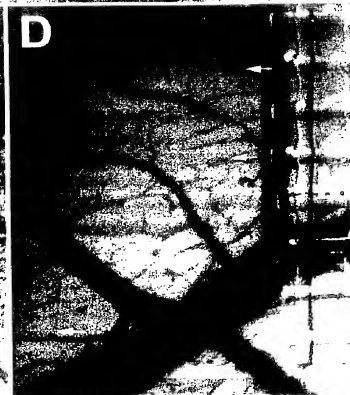
FIG. 30D

FIG. 31A   FIG. 31B   FIG. 31C   FIG. 31D
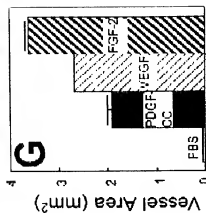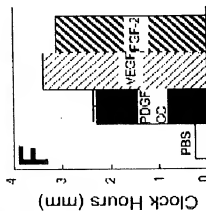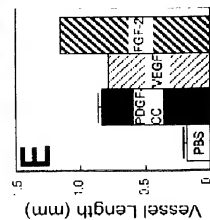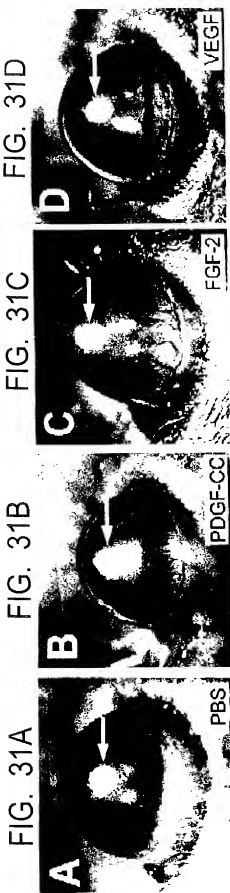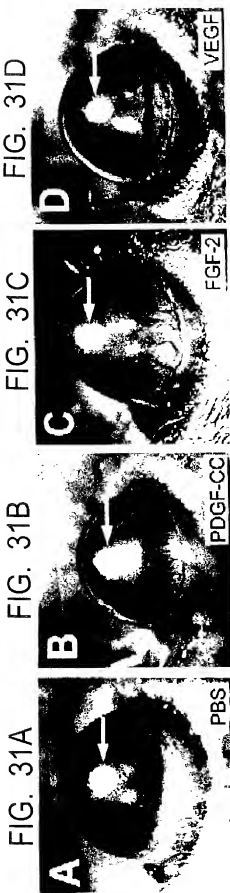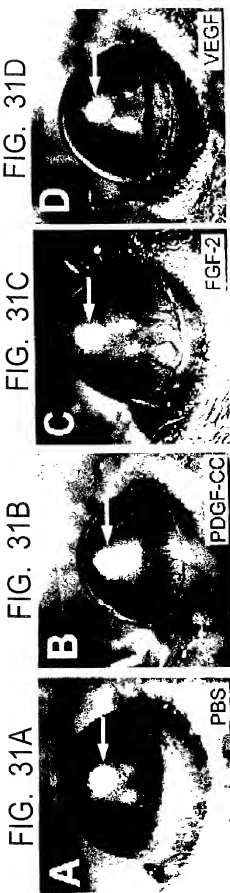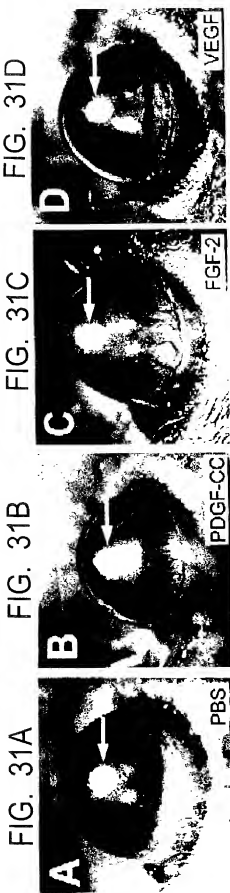
FIG. 31E   FIG. 31F   FIG. 31G
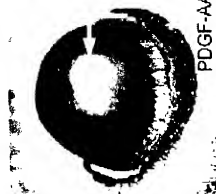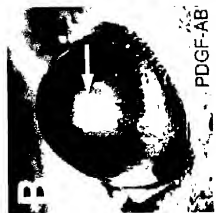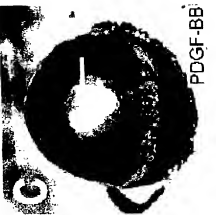
FIG. 32A FIG. 32B FIG. 32C FIG. 32D
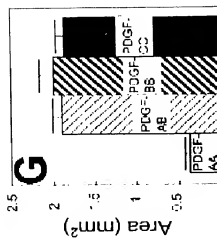PDGF-AA PDGF-AB PDGF-BB PDGF-CC
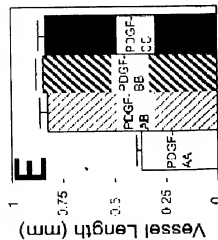
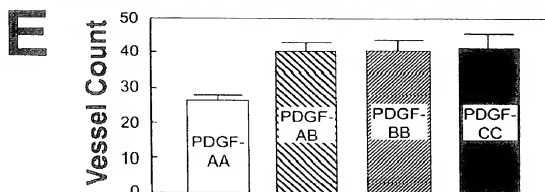FIG. 32E FIG. 32F FIG. 32G

FIG. 33A

FIG. 33B

FIG. 33C

FIG. 33D

FIG. 33E